

*Campbell*  
*Barbara*  
 PCT

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/830,807

DATE: 05/18/2001  
 TIME: 11:03:12

Input Set : A:\gje-65.txt  
 Output Set: N:\CRF3\05182001\I830807.raw

**ENTERED**

#5  
 P4  
 10-12-01

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3 <110> APPLICANT: Crooke, Helen R.
4   Clarke, Enda E.
5   Everest, Paul H.
6   Dougan, Gordon
7   Holden, David W.
8   Shea, Jacqueline E.
9   Feldman, Robert G.
11 <120> TITLE OF INVENTION: VIRULENCE GENES AND PROTEINS, AND THEIR USE
13 <130> FILE REFERENCE: GJE-65
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/830,807
C--> 16 <141> CURRENT FILING DATE: 2001-04-30
18 <160> NUMBER OF SEQ ID NOS: 72
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4333
24 <212> TYPE: DNA
25 <213> ORGANISM: Escherichia coli
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1017)..(2549)
31 <400> SEQUENCE: 1
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34 atgccgaggc acaaaaaaaaa caccgatagt ttaccatcg agaatttttt attcgtttta 120
36 tcagaatttt ctaaattatt tctgatacgt ttgaatatcc agacgcacag cgtcgtcatg 180
38 accactaaca ccagtaaaaaa ccacaggtgt gatattaatt cccaggccaa cgtattatat 240
40 ttgtcataca atgacagtcc aggccaaact tccgctttcc ctttgacgta ttgcagcata 300
42 ataaattgcg gcaatgtcag tagggggatg gctgttaaca tcgggatacc tacacgttcg 360
44 acacgtactt tccaccattt tttcaaggga tagcgtaaaa aaagcatgta ggaaaagtac 420
46 ccgatataaa cgaaaaatac ctgcatgcgg aacgagtgga tgaagtcatt aaaaagggtc 480
48 agccataatg acggttcggc gctattcaca tgccatgtat ggctcgaata gattaaagaa 540
50 atatgaaaag ggatccctaa caacatcagc caggcgcgga tggagtcgag gaaatattca 600
52 cgttgcgcgg gtactgggtt catatatggt taactaatct cgattttttc gtcttatccc 660
54 tgtegggtta tgccttttagg cttgttgcca tagcgacacc gacctgaccg cgccaggcgc 720
56 aggcttcaag gtttttatgc atagcatcat cgctaccact aaccagaatg gaagcgtctg 780
57 taagacggtt gataaataaa tttgctggca aaccctacac gaagtcgatg cttctgtctt 840
59 taggagaagc acggaaagtg aaaacggttg caatcagggt cttaatccat gagccagtgt 900
61 gctgaacgat accgggattc tgttgcgga atggcagggt atccattaaa atagatcgga 960
63 tcgatataag cacacaaaagg gggaagtgtt tactaattat gaaacataaa ctacaa atg 1019
64                                     Met
65                                     1
67 atg aaa atg cgt tgg ttg agt gct gca gta atg tta acc ctg tat aca 1067
68 Met Lys Met Arg Trp Leu Ser Ala Ala Val Met Leu Thr Leu Tyr Thr
69          5          10          15
71 tct tca agc tgg gct ttc agt att gat gtc gca aag caa gct caa 1115
72 Ser Ser Ser Trp Ala Phe Ser Ile Asp Asp Val Ala Lys Gln Ala Gln
73          20          25          30
75 tcc tta gcc ggg aaa ggc tat gag gcg ccc aaa agc aac ttg ccc tcc 1163

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76 Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro Ser
77      35      40      45
79 gtt ttc cgc gat atg aaa tac gcg gac tat cag cag atc cag ttt aat 1211
80 Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe Asn
81 50      55      60      65
83 cat gac aaa gcg tac tgg aac aat ctg aag acc cca ttc aaa ctc gag 1259
84 His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu Glu
85      70      75      80
87 ttc tac cat cag ggt atg tac ttc gat acc ccg gtc aaa ata aat gaa 1307
88 Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn Glu
89      85      90      95
91 gtg act gcc acc gca gtc aaa cga atc aaa tac agc ccg gat tat ttc 1355
92 Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr Phe
93      100      105      110
95 act ttc ggc gat gtt cag cat gac aaa gac acg gta aaa gac ctt ggt 1403
96 Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu Gly
97      115      120      125
99 ttt gcc ggt ttc aaa gtg ctt tac ccg atc aac agc aaa gat aaa aac 1451
100 Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys Asn
101 130      135      140      145
103 gat gaa atc gtc agc atg ctc ggg gcc agc tat ttc cgc gtg att ggt 1499
104 Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile Gly
105      150      155      160
107 gca ggt cag gtt tat ggc ctt tct gca cgc ggc ctg gca att gat acc 1547
108 Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp Thr
109      165      170      175
111 gcc ttg cca tcg ggt gaa gaa ttt cca cgc ttc aaa gag ttc tgg atc 1595
112 Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp Ile
113      180      185      190
115 gag cgt cca aaa ccg act gat aaa cgt tta acc att tat gca ttg ctt 1643
116 Glu Arg Pro Lys Pro Thr Asp Lys Arg Leu Thr Ile Tyr Ala Leu Leu
117      195      200      205
119 gac tcg ccg cgc gcg aca ggt gct tac aaa ttc gta gtt atg cca gga 1691
120 Asp Ser Pro Arg Ala Thr Gly Ala Tyr Lys Phe Val Val Met Pro Gly
121 210      215      220      225
123 cgt gac acg gtt gtg gat gtg cag tcg aaa atc tat ctg cgc gat aaa 1739
124 Arg Asp Thr Val Val Asp Val Gln Ser Lys Ile Tyr Leu Arg Asp Lys
125      230      235      240
127 gtc ggc aaa ctg ggg gtt gca ccg tta acc agt atg ttc ctg ttt ggg 1787
128 Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe Gly
129      245      250      255
131 ccg aac caa ccg tcg cct gca aat aac tat cgt ccg gag ttg cac gac 1835
132 Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His Asp
133      260      265      270
135 tct aac ggt ctg tct atc cat gct ggt aat ggc gaa tgg atc tgg cgt 1883
136 Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp Arg
137      275      280      285
139 ccg ttg aat aac ccg aaa cat tta gcg gtc agc agc ttc tcg atg gaa 1931
140 Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met Glu

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141 290          295          300          305
143 aac ccg caa ggc ttc ggt cta ttg cag cgt ggt cgt gat ttc tcc cgc 1979
144 Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser Arg
145          310          315          320
147 ttt gaa gat ctc gat gat cgt tac gat ctt cgt cca agc gca tgg gtg 2027
148 Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp Val
149          325          330          335
151 act ccg aaa ggg gag tgg ggc aaa ggc agc gtt gag ctg gtg gaa att 2075
152 Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu Ile
153          340          345          350
155 cca acc aac gat gaa acc aac gat aac atc gtc gct tac tgg acg ccg 2123
156 Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr Pro
157          355          360          365
159 gat cag ctg ccg gag ccg ggt aaa gag atg aac ttt aaa tac acc atc 2171
160 Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr Ile
161 370          375          380          385
163 acc ttc agc cgt gat gaa gac aaa ctg cat gcg cca gat aac gca tgg 2219
164 Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala Trp
165          390          395          400
167 gtg caa caa acg cgt cgt tca acg ggg gat gtg aag cag tgc aac ctg 2267
168 Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn Leu
169          405          410          415
171 att cgc cag cct gac ggt act atc gcc ttt gtg gtc gat ttt acc ggc 2315
172 Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr Gly
173          420          425          430
175 gct gag atg aaa aaa ctg cca gag gat acc ccg gtc aca gcg caa acc 2363
176 Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln Thr
177          435          440          445
179 agc att ggt gat aat ggt gag ata gtt gaa agc acg gtg cgt tat aac 2411
180 Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr Asn
181 450          455          460          465
183 ccg gtt acc aaa ggc tgg cgt ctg gtg atg cgt gtg aaa gtg aaa gat 2459
184 Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys Asp
185          470          475          480
187 gcc aag aaa acc act gaa atg cgt gct gcg ctg gtg aat gcc gat cag 2507
188 Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp Gln
189          485          490          495
191 acg ttg agt gaa acc tgg agc tac cag tta cct gcc aat gaa 2549
192 Thr Leu Ser Glu Thr Trp Ser Tyr Gln Leu Pro Ala Asn Glu
193          500          505          510
195 taagacaact gactacattg acgcaatgcc catcgccgca agcgagaaaag cggcattgcc 2609
197 gaagactgat atccgcgcgcg ttcacacaggc gctggatgcc gaacaccgca cctgggcgcg 2669
199 ggaggatgac tccccgcaag gctcggtaaa ggcgcgtctg gaacaagcct ggccagattc 2729
201 acttgctgat ggacagttaa ttaaagacga cgaaggggcg gatcagctaa aggcgatgcc 2789
203 agaagtaaaa cgctcctcga tgtttcccga cccgtggcgt accaaccggt taggcggttt 2849
205 ctgggatcgc ctgcgtggac gcgatgtgac gccgcgctat ctggctcgtt tgaccaaaga 2909
207 agagcaggag agtgagcaaa agtggcggtac cgtcgggtacc atccgcggtt acattctgtt 2969
209 gatcctgacg ctgcgcgcaaa ctgttgcgc gacctgggtat atgaagacca ttcttcctta 3029
211 tcaggggtgg gcgctgatta atcctatgga tatggttggt caggatgtgt gggtttcctt 3089

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213 tatgcagctt ctgccttata tgctgcaaac cggatccctg atcctctttg cggacttggt 3149
215 ctgttgggtg tccgccggat tctggaccgg cgttgatggg cttcctgcaa ctgcttattg 3209
217 gtcgcgataa atacagtata tctgcgtcaa cagttggcga tgaaccatta aaccgggagc 3269
219 atcgcacggc gttgatcatg cctatctgta acgaagacgt gaaccgtgtt ttgctggct 3329
221 tgcgtgcaac gtgggaatca gtaaaagcca ccgggaatgc caaacathtt gatgtctaca 3389
223 ttcttagtga cagttataac ccgatatctt gcgtcgaga gcaaaaagcc tggatggagc 3449
225 ttatcgctga agtcgggtgc gaaggtcaga tttctatcg ccgccgccgc cgtcgctga 3509
227 agcgtaaaag cggtaaatat gatgacttct gccgtcgctg gggcagccag tacagctaca 3569
229 tgggtgggtg ggtgctgac tcggtaatga ccggtgattg tttgtgcggc ctggtgcgcc 3629
231 tgatggaagc caaccgaac gccgggatca ttcagtcgtc gccgaaagcg tccggcatgg 3689
233 atacgctgta tgcgcgctgt cagcagttcg cgaccgcgt gtatgggcca ctgtttacag 3749
235 ccggtttgca cttctggcaa cttggcgagt cgcactactg ggggcataac gcgattatcc 3809
237 gcgtgaaacc gtttatcgag cactgtgcac tggctccgct gccggcgcaa ggttctttt 3869
239 ccggttcaat cctgtcacat gacttcgtgg aagcggcgtt gatgcgccgt gcagggttgg 3929
241 ggggtctgat tgcttacgat ctcccgggtt cttatgaaga attaccgctt aacttgctt 3989
243 atgagctaaa acgtgaccgc cgctggtgcc acggtaacct gatgaacttc cgtctgttcc 4049
245 tgggtgaagg tatgcacccg gttcacccgt cgggttctct gacggcgctg atgtcttatc 4109
247 tctccgctcc gctgtggttt atgttctctc cgctctctac tgcattgcag gtagtacatg 4169
249 cggtgaccga accgcaatac ttcctgcaac cacggcagtt gttcccggta tggccgcagt 4229
251 ggcgtcctga gctggcgatt gcactttttg cttcgaccat ggtgctgttg ttctgcca 4289
253 agctattgag cattttgctt atctggtgca aaggaacgaa agaa 4333

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256 &lt;210&gt; SEQ ID NO: 2

257 &lt;211&gt; LENGTH: 511

258 &lt;212&gt; TYPE: PRT

259 &lt;213&gt; ORGANISM: Escherichia coli

261 &lt;400&gt; SEQUENCE: 2

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262 Met Met Lys Met Arg Trp Leu Ser Ala Ala Val Met Leu Thr Leu Tyr
263 1 5 10 15
265 Thr Ser Ser Ser Trp Ala Phe Ser Ile Asp Asp Val Ala Lys Gln Ala
266 20 25 30
268 Gln Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro
269 35 40 45
271 Ser Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe
272 50 55 60
274 Asn His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu
275 65 70 75 80
277 Glu Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn
278 85 90 95
280 Glu Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr
281 100 105 110
283 Phe Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu
284 115 120 125
286 Gly Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys
287 130 135 140
289 Asn Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile
290 145 150 155 160
292 Gly Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp
293 165 170 175
295 Thr Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp

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296          180          185          190
298 Ile Glu Arg Pro Lys Pro Thr Asp Lys Arg Leu Thr Ile Tyr Ala Leu
299          195          200          205
301 Leu Asp Ser Pro Arg Ala Thr Gly Ala Tyr Lys Phe Val Val Met Pro
302          210          215          220
304 Gly Arg Asp Thr Val Val Asp Val Gln Ser Lys Ile Tyr Leu Arg Asp
305 225          230          235          240
307 Lys Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe
308          245          250          255
310 Gly Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His
311          260          265          270
313 Asp Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp
314          275          280          285
316 Arg Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met
317          290          295          300
319 Glu Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser
320 305          310          315          320
322 Arg Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp
323          325          330          335
325 Val Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu
326          340          345          350
328 Ile Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr
329          355          360          365
331 Pro Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr
332          370          375          380
334 Ile Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala
335 385          390          395          400
337 Trp Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn
338          405          410          415
340 Leu Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr
341          420          425          430
343 Gly Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln
344          435          440          445
346 Thr Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr
347          450          455          460
349 Asn Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys
350 465          470          475          480
352 Asp Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp
353          485          490          495
355 Gln Thr Leu Ser Glu Thr Trp Ser Tyr Gln Leu Pro Ala Asn Glu
356          500          505          510

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360 &lt;210&gt; SEQ ID NO: 3

361 &lt;211&gt; LENGTH: 574

362 &lt;212&gt; TYPE: DNA

363 &lt;213&gt; ORGANISM: Escherichia coli

365 &lt;400&gt; SEQUENCE: 3

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366 ttctgttgatc ctgtcacccgt ttgttcgggt atttccagcc gtgccaccgt tggctctgca 60
367 accaaacgct ggaaactgtt cctgatccc ggaagagtat tcaccgccgc aggtgctggt 120
368 tgataccgat cggttccttg agatgaatcg tcaatgctcc cttgatgatg gttttatgca 180

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## VERIFICATION SUMMARY

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Input Set : A:\gje-65.txt

Output Set: N:\CRF3\05182001\I830807.raw

L:15 M:270 C: Current Application Number differs, Replaced Application Number  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:891 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:895 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:907 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:915 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:919 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:927 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:931 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:935 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:939 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:943 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:947 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
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L:979 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:983 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:987 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:991 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:995 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:999 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1003 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1019 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1023 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:1047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10

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L:2426 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

L:2430 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

L:2434 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

L:2438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27